SEQUENCE LISTING

<110> Lowery, David E.
Smith, Valdin G.
Kubiak, Teresa M.
Larsen, Martha J.

<120> Drosophila G Protein Coupled Receptors, Nucleic Acids, and Methods Related to the Same

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<141> 2005-02-04

<150> US 10/283,423
<151> 2002-10-30

<150> US 09/693,746
<151> 2000-10-20

<150> US 09/425,676
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Asn Val Leu Val Cys Tyr Val Val Leu Arg Asn Arg Ala Met Gln Thr
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Val Thr Asn Ile Phe Ile Thr Asn Leu Ala Leu Ser Asp Ile Leu Leu
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Cys Val Leu Ala Val Pro Phe Thr Pro Leu Tyr Thr Phe Met Gly Arg
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Arg Tyr Phe Val Ile Ile Tyr Pro Phe His Pro Arg Met Lys Leu Ser
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Thr Cys Ile Gly Ile Ile Val Ser Ile Trp Val Ile Ala Leu Leu Ala
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Thr Val Pro Tyr Gly Met Tyr Met Lys Met Thr Asn Glu Leu Val Asn
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Tyr Gly Asn Gly Thr Gly Ala Val Ser Pro Ile Leu Ser Gly Arg Gly
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545 550 555 560

Thr Thr Gly Ile Ser Ile Leu Glu Thr Ser Thr Ser His Cys Gln Asp
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Ala Ile Thr Gly Phe Phe Gly Asn Leu Leu Val Ile Leu Val Val Val
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Phe Asn Asn Asn Met Arg Ser Thr Thr Asn Leu Met Ile Val Asn Leu
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His Asp Val Val Val Asp Tyr Asp Ala Lys Lys Asn Ile Thr Tyr Gly
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Met Cys Thr Phe Thr Thr Asn Asp Phe Leu Gly Pro Arg Thr Tyr Gln
195 200 205

Val Thr Phe Phe Ile Ser Ser Tyr Leu Leu Pro Leu Met Ile Ile Ser
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Gly Leu Tyr Met Arg Met Ile Met Arg Leu Trp Arg Gln Gly Thr Gly
225 230 235 240

Val Arg Met Ser Lys Glu Ser Gln Arg Gly Arg Lys Arg Val Thr Arg
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260 265 270

Gln Leu Ile Leu Leu Leu Lys Ser Leu Asp Val Ile Glu Thr Asn Thr
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Leu Thr Lys Leu Val Ile Gln Val Thr Ala Gln Thr Leu Ala Tyr Ser
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Ser Ser Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Ser Glu Asn Phe
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Ala Ile Asn Thr Ser Asp Leu Asn Glu Thr Gly Ser Arg Pro Leu Asp
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Pro Val Leu Ile Asp Arg Phe Leu Ser Asn Arg Ala Val Asp Ser Pro
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Trp Tyr His Met Leu Ile Ser Met Tyr Gly Val Leu Ile Val Phe Gly
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Ser Lys Tyr Trp Pro Tyr Gly Ser Cys Ser Ile Leu Cys Lys Thr Ile
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Ile Pro Tyr Cys Ile Glu Asp Trp Pro Ser Arg Asn Gly Arg Phe Tyr
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Ala Ile Thr Gly Phe Phe Gly Asn Leu Leu Val Ile Leu Val Val Val
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Phe Asn Asn Asn Met Arg Ser Thr Thr Asn Leu Met Ile Val Asn Leu
65 70 75 80

Ala Ala Ala Asp Leu Met Phe Val Ile Leu Cys Ile Pro Phe Thr Ala
85 90 95

Thr Asp Tyr Met Val Tyr Tyr Trp Pro Tyr Gly Arg Phe Trp Cys Arg
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Ser Val Gln Tyr Leu Ile Val Val Thr Ala Phe Ala Ser Ile Tyr Thr
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Leu Val Leu Met Ser Ile Asp Arg Phe Leu Ala Val Val His Pro Ile
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Thr Leu Trp Ile Val Val Leu Val Val Ser Val Pro Val Ala Phe Thr
165 170 175

His Asp Val Val Val Asp Tyr Asp Ala Lys Lys Asn Ile Thr Tyr Gly
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Met Cys Thr Phe Thr Thr Asn Asp Phe Leu Gly Pro Arg Thr Tyr Gln
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Val Thr Phe Phe Ile Ser Ser Tyr Leu Leu Pro Leu Met Ile Ile Ser
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Gly Leu Tyr Met Arg Met Ile Met Arg Leu Trp Arg Gln Gly Thr Gly
225 230 235 240

Val Arg Met Ser Lys Glu Ser Gln Arg Gly Arg Lys Arg Val Thr Arg
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Leu Thr Lys Leu Val Ile Gln Val Thr Ala Gln Thr Leu Ala Tyr Ser
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Trp Ser Asn Trp Ser Asn Trp Ser Thr Pro Ala Gly Val Leu Phe Ser
            20                  25                  30

Ala Met Ser Ser Val Leu Ser Ala Ser Asn His Thr Pro Leu Pro Asp
        35                  40                  45

Phe Gly Gln Glu Leu Ala Leu Ser Thr Ser Ser Phe Asn His Ser Gln
    50                  55                  60

Thr Leu Ser Thr Asp Gln Pro Ala Val Gly Asp Val Glu Asp Ala Ala
65                  70                  75                  80

Glu Asp Ala Ala Ala Ser Met Glu Thr Gly Ser Phe Ala Phe Val Val
                85                  90                  95

Pro Trp Trp Arg Gln Val Leu Trp Ser Ile Leu Phe Gly Gly Met Val
            100                 105                 110

Ile Val Ala Thr Gly Gly Asn Leu Ile Val Val Trp Ile Val Met Thr
        115                 120                 125

Thr Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Ile Val Asn Leu Ser
    130                 135                 140

Ile Ala Asp Ala Met Val Ser Ser Leu Asn Val Thr Phe Asn Tyr Tyr
145                 150                 155                 160

Tyr Met Leu Asp Ser Asp Trp Pro Phe Gly Glu Phe Tyr Cys Lys Leu
                165                 170                 175

Ser Gln Phe Ile Ala Met Leu Ser Ile Cys Ala Ser Val Phe Thr Leu
            180                 185                 190

Met Ala Ile Ser Ile Asp Arg Tyr Val Ala Ile Ile Arg Pro Leu Gln
        195                 200                 205

Pro Arg Met Ser Lys Arg Cys Asn Leu Ala Ile Ala Ala Val Ile Trp
    210                 215                 220

Leu Ala Ser Thr Leu Ile Ser Cys Pro Met Met Ile Ile Tyr Arg Thr
225                 230                 235                 240
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Glu Glu Val Pro Val Arg Gly Leu Ser Asn Arg Thr Val Cys Tyr Pro
245 250 255

Glu Trp Pro Asp Gly Pro Thr Asn His Ser Thr Met Glu Ser Leu Tyr
260 265 270

Asn Ile Leu Ile Ile Ile Leu Thr Tyr Phe Leu Pro Ile Val Ser Met
275 280 285

Thr Val Thr Tyr Ser Arg Val Gly Ile Glu Leu Trp Gly Ser Lys Thr
290 295 300

Ile Gly Glu Cys Thr Pro Arg Gln Val Glu Asn Val Arg Ser Lys Arg
305 310 315 320

Arg Val Val Lys Met Met Ile Val Val Val Leu Ile Phe Ala Ile Cys
325 330 335

Trp Leu Pro Phe His Ser Tyr Phe Ile Ile Thr Ser Cys Tyr Pro Ala
340 345 350

Ile Thr Glu Ala Pro Phe Ile Gln Glu Leu Tyr Leu Ala Ile Tyr Trp
355 360 365

Leu Ala Met Ser Asn Ser Met Tyr Asn Pro Ile Ile Tyr Cys Trp Met
370 375 380

Asn Ser Arg Phe Arg Tyr Gly Phe Lys Met Val Phe Arg Trp Cys Leu
385 390 395 400

Phe Val Arg Val Gly Thr Glu Pro Phe Ser Arg Arg Glu Asn Leu Thr
405 410 415

Ser Arg Tyr Ser Cys Ser Gly Ser Pro Asp His Asn Arg Ile Lys Arg
420 425 430

Asn Asp Thr Gln Lys Ser Ile Leu Tyr Thr Cys Pro Ser Ser Pro Lys
435 440 445

Ser His Arg Ile Ser His Ser Gly Thr Gly Arg Ser Ala Thr Leu Arg
450 455 460

Asn Ser Leu Pro Ala Glu Ser Leu Ser Ser Gly Gly Ser Gly Gly Gly
465 470 475 480

Gly His Arg Lys Arg Leu Ser Tyr Gln Gln Glu Met Gln Gln Arg Trp
485 490 495

Ser Gly Pro Asn Ser Ala Thr Ala Val Thr Asn Ser Ser Ser Thr Ala
500 505 510

Asn Thr Thr Gln Leu Leu Ser
515

<210> 11
<211> 1568
<212> DNA
<213> D. melanogaster

<400> 11
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agcaattgga gcaactggag cacccccgcc ggcgtccttt tctcggccat gagcagcgtg 120

ctctcggcca gcaaccatac gcctctgccg gactttggcc aggagctcgc cctatccacc 180

agctccttca atcacagcca gaccctatcc accgacctgc ccgccgtcgg ggacgtggaa 240

gacgcggccg aggatgcggc ggcgtccatg gagacgggct cgtttgcatt tgtggtcccg 300

tggtggcgtc aggtgctctg gagcatcctc ttcggcggca tggtcattgt ggcgacgggc 360

ggtaacctga ttgttgtctg gatcgtgatg acgaccaagc ggatgcggac ggtaaccaac 420

tatttcatag taaatctctc catcgcggac gccatggtgt ccagcctgaa cgtcaccttc 480

aactactact acatgctgga tagcgactgg cccttcggcg agttctactg caagttgtcc 540

cagttcatcg cgatgctaag catctgcgcc tcagtgttca ccctaatggc catctccatc 600

gacagatacg tggccatcat ccggccactg cagccgcgga tgagcaagcg gtgcaacctg 660

gccatcgcgg cggtcatctg gctggcctcc acgctcatct cctgccccat gatgatcatc 720

taccgcacgg aggaggtgcc ggtccgcggg ctcagcaacc gcacggtctg ctacccggag 780

tggcccgatg ggcccaccaa tcactccacg atggagtccc tctacaacat cctcatcatc 840

attctaacct acttcctgcc catcgtctcc atgacggtca cctactcgcg cgtgggcatc 900

gagctctggg gatccaagac catcggcgag tgcacgcccc gccaggtgga gaatgtgcgg 960

agtaagcgaa gggtggtgaa gatgatgatt gtggtcgtcc tgatattcgc catctgctgg 1020

ctgccgttcc acagctactt cataatcaca tcctgctacc cggccatcac ggaggcgccc 1080

ttcatccagg aactttacct ggccatctac tggctggcca tgagcaactc catgtacaat 1140

cccattatat actgctggat gaattcgcgc tttcgctatg gtttcaagat ggtcttccgc 1200

tggtgcctgt ttgtgcgcgt gggcactgaa ccctttagtc ggcgggagaa cctgacatcc 1260

cggtactcct gctccggttc cccggatcac aatcgcatca agcgcaatga tacccagaaa 1320

tcgatacttt atacctgtcc cagctcaccc aagtcgcatc gaatttcgca cagcggaaca 1380

ggtcgcagtg cgacgctgag gaacagtctg ccggcggagt cattgtcgtc cggtggatct 1440

ggaggtggag gacacaggaa acggttgtcc taccagcagg aaatgcagca gcggtggtca 1500

ggacccaata gtgccaccgc agtgaccaat tccagcagta cggccaacac cacccaactg 1560

ctctcctg 1568

<210> 12
<211> 522
<212> PRT
<213> D. melanogaster

<400> 12

Met Glu Asn Arg Ser Asp Phe Glu Ala Asp Asp Tyr Gly Asp Ile Ser
1 5 10 15

Trp Ser Asn Trp Ser Asn Trp Ser Asn Trp Ser Thr Pro Ala Gly Val
20 25 30

Leu Phe Ser Ala Met Ser Ser Val Leu Ser Ala Ser Asn His Thr Pro
35 40 45

Leu Pro Asp Phe Gly Gln Glu Leu Ala Leu Ser Thr Ser Ser Phe Asn
50 55 60

His Ser Gln Thr Leu Ser Thr Asp Leu Pro Ala Val Gly Asp Val Glu
65 70 75 80

Asp Ala Ala Glu Asp Ala Ala Ala Ser Met Glu Thr Gly Ser Phe Ala
85 90 95

Phe Val Val Pro Trp Trp Arg Gln Val Leu Trp Ser Ile Leu Phe Gly
100 105 110

Gly Met Val Ile Val Ala Thr Gly Gly Asn Leu Ile Val Val Trp Ile
115 120 125

```
Val Met Thr Thr Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Ile Val
    130                 135                 140

Asn Leu Ser Ile Ala Asp Ala Met Val Ser Ser Leu Asn Val Thr Phe
145                 150                 155                 160

Asn Tyr Tyr Tyr Met Leu Asp Ser Asp Trp Pro Phe Gly Glu Phe Tyr
                165                 170                 175

Cys Lys Leu Ser Gln Phe Ile Ala Met Leu Ser Ile Cys Ala Ser Val
            180                 185                 190

Phe Thr Leu Met Ala Ile Ser Ile Asp Arg Tyr Val Ala Ile Ile Arg
        195                 200                 205

Pro Leu Gln Pro Arg Met Ser Lys Arg Cys Asn Leu Ala Ile Ala Ala
    210                 215                 220

Val Ile Trp Leu Ala Ser Thr Leu Ile Ser Cys Pro Met Met Ile Ile
225                 230                 235                 240

Tyr Arg Thr Glu Glu Val Pro Val Arg Gly Leu Ser Asn Arg Thr Val
                245                 250                 255

Cys Tyr Pro Glu Trp Pro Asp Gly Pro Thr Asn His Ser Thr Met Glu
            260                 265                 270

Ser Leu Tyr Asn Ile Leu Ile Ile Ile Leu Thr Tyr Phe Leu Pro Ile
        275                 280                 285

Val Ser Met Thr Val Thr Tyr Ser Arg Val Gly Ile Glu Leu Trp Gly
    290                 295                 300

Ser Lys Thr Ile Gly Glu Cys Thr Pro Arg Gln Val Glu Asn Val Arg
305                 310                 315                 320

Ser Lys Arg Arg Val Val Lys Met Met Ile Val Val Val Leu Ile Phe
                325                 330                 335

Ala Ile Cys Trp Leu Pro Phe His Ser Tyr Phe Ile Ile Thr Ser Cys
            340                 345                 350
```

Tyr Pro Ala Ile Thr Glu Ala Pro Phe Ile Gln Glu Leu Tyr Leu Ala
355 360 365

Ile Tyr Trp Leu Ala Met Ser Asn Ser Met Tyr Asn Pro Ile Ile Tyr
370 375 380

Cys Trp Met Asn Ser Arg Phe Arg Tyr Gly Phe Lys Met Val Phe Arg
385 390 395 400

Trp Cys Leu Phe Val Arg Val Gly Thr Glu Pro Phe Ser Arg Arg Glu
405 410 415

Asn Leu Thr Ser Arg Tyr Ser Cys Ser Gly Ser Pro Asp His Asn Arg
420 425 430

Ile Lys Arg Asn Asp Thr Gln Lys Ser Ile Leu Tyr Thr Cys Pro Ser
435 440 445

Ser Pro Lys Ser His Arg Ile Ser His Ser Gly Thr Gly Arg Ser Ala
450 455 460

Thr Leu Arg Asn Ser Leu Pro Ala Glu Ser Leu Ser Ser Gly Gly Ser
465 470 475 480

Gly Gly Gly Gly His Arg Lys Arg Leu Ser Tyr Gln Gln Glu Met Gln
485 490 495

Gln Arg Trp Ser Gly Pro Asn Ser Ala Thr Ala Val Thr Asn Ser Ser
500 505 510

Ser Thr Ala Asn Thr Thr Gln Leu Leu Ser
515 520

<210> 13
<211> 1394
<212> DNA
<213> D. melanogaster

<400> 13
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ccggaccctg catccttact ttacaatacc accgcactgc cagcggacga tgaagggtcc 180

aactatggat atggctccac cacaacgctc agtggcctcc agttcgagac ctataatatc 240

actgtgatga tgaactttag ctgtgacgac tatgaccttc tatcggagga catgtggtct 300

agtgcctact ttaagatcat cgtctacatg ctctacattc ccatctttat cttcgccctg 360

atcggcaacg gaacggtctg ctatatcgtc tattccacac ctcgcatgcg cacggtcacc 420

aattacttta tagccagctt ggccatcggc gacatcctga tgtccttctt ctgcgttccg 480

tcgtccttca tctcgctgtt catcctgaac tactggcctt ttggcctggc cctctgtcac 540

tttgtgaact actcgcaggc ggtctcagtt ctggtcagcg cctatacttt ggtggcaatt 600

agcattgacc gctacatagc cattatgtgg ccattaaagc cacgcatcac aaaacgctat 660

gccaccttca tcatcgccgg cgtttggttt attgcacttg ccaccgcact tcccataccc 720

atcgtctctg gactcgacat cccaatgtcg ccgtggcaca cgaaatgcga gaaatacatt 780

tgccgcgaaa tgtggccgtc gcggacgcag gagtactact acaccctgtc cctcttcgcg 840

ctgcagttcg tcgtgccgct gggcgtgctc atcttcacct acgcccggat caccattcgc 900

gtctgggcga aacgaccgcc aggcgaggcg gaaaccaacc gcgaccagcg gatggcacgc 960

tccaaacgga agatggtcaa aatgatgctg acggttgtga ttgtgttcac ctgctgttgg 1020

ctgcccttca tatttttgca gcttttactg aacgacgagg agttcgccca ctgggatcct 1080

ctgccgtatg tatggttcgc gtttcactgg ctggccatgt cgcactgctg ctacaatccg 1140

atcatctact gctacatgaa cgcccgtttc aggagcggat tcgtccagct gatgcaccgt 1200

atgcccggcc tgcgtcgctg gtgctgcctg cggagcgtcg gtgatcgcat gaacgcaact 1260

tccggaacgg gtccagcact tcctctcaat cgaatgaaca catccaccac ctacatcagc 1320

gctcgtcgaa agccacgagc gacatctttg cgagcgaacc cattatcatg cggcgagacg 1380

tcaccactgc ggta 1394

<210> 14
<211> 464
<212> PRT
<213> D. melanogaster

<400> 14

Met Glu His His Asn Ser His Leu Leu Pro Gly Gly Ser Glu Lys Met
1 5 10 15

Tyr Tyr Ile Ala His Gln Gln Pro Met Leu Arg Asn Glu Asp Asp Asn
20 25 30

Tyr Gln Glu Gly Tyr Phe Ile Arg Pro Asp Pro Ala Ser Leu Leu Tyr
35 40 45

Asn Thr Thr Ala Leu Pro Ala Asp Asp Glu Gly Ser Asn Tyr Gly Tyr
50 55 60

Gly Ser Thr Thr Thr Leu Ser Gly Leu Gln Phe Glu Thr Tyr Asn Ile
65 70 75 80

Thr Val Met Met Asn Phe Ser Cys Asp Asp Tyr Asp Leu Leu Ser Glu
85 90 95

Asp Met Trp Ser Ser Ala Tyr Phe Lys Ile Ile Val Tyr Met Leu Tyr
100 105 110

Ile Pro Ile Phe Ile Phe Ala Leu Ile Gly Asn Gly Thr Val Cys Tyr
115 120 125

Ile Val Tyr Ser Thr Pro Arg Met Arg Thr Val Thr Asn Tyr Phe Ile
130 135 140

Ala Ser Leu Ala Ile Gly Asp Ile Leu Met Ser Phe Phe Cys Val Pro
145 150 155 160

Ser Ser Phe Ile Ser Leu Phe Ile Leu Asn Tyr Trp Pro Phe Gly Leu
165 170 175

Ala Leu Cys His Phe Val Asn Tyr Ser Gln Ala Val Ser Val Leu Val
180 185 190

Ser Ala Tyr Thr Leu Val Ala Ile Ser Ile Asp Arg Tyr Ile Ala Ile
195 200 205

Met Trp Pro Leu Lys Pro Arg Ile Thr Lys Arg Tyr Ala Thr Phe Ile
210 215 220

Ile Ala Gly Val Trp Phe Ile Ala Leu Ala Thr Ala Leu Pro Ile Pro
225 230 235 240

Ile Val Ser Gly Leu Asp Ile Pro Met Ser Pro Trp His Thr Lys Cys
245 250 255

```
Glu Lys Tyr Ile Cys Arg Glu Met Trp Pro Ser Arg Thr Gln Glu Tyr
            260                 265                 270

Tyr Tyr Thr Leu Ser Leu Phe Ala Leu Gln Phe Val Val Pro Leu Gly
        275                 280                 285

Val Leu Ile Phe Thr Tyr Ala Arg Ile Thr Ile Arg Val Trp Ala Lys
    290                 295                 300

Arg Pro Pro Gly Glu Ala Glu Thr Asn Arg Asp Gln Arg Met Ala Arg
305                 310                 315                 320

Ser Lys Arg Lys Met Val Lys Met Met Leu Thr Val Val Ile Val Phe
                325                 330                 335

Thr Cys Cys Trp Leu Pro Phe Asn Ile Leu Gln Leu Leu Leu Asn Asp
            340                 345                 350

Glu Glu Phe Ala His Trp Asp Pro Leu Pro Tyr Val Trp Phe Ala Phe
        355                 360                 365

His Trp Leu Ala Met Ser His Cys Cys Tyr Asn Pro Ile Ile Tyr Cys
    370                 375                 380

Tyr Met Asn Ala Arg Phe Arg Ser Gly Phe Val Gln Leu Met His Arg
385                 390                 395                 400

Met Pro Gly Leu Arg Arg Trp Cys Cys Leu Arg Ser Val Gly Asp Arg
                405                 410                 415

Met Asn Ala Thr Ser Gly Thr Gly Pro Ala Leu Pro Leu Asn Arg Met
            420                 425                 430

Asn Thr Ser Thr Thr Tyr Ile Ser Ala Arg Arg Lys Pro Arg Ala Thr
        435                 440                 445

Ser Leu Arg Ala Asn Pro Leu Ser Cys Gly Glu Thr Ser Pro Leu Arg
    450                 455                 460
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<210> 15
<211> 1556
<212> DNA
<213> D. melanogaster

<400> 15
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ccggaccctg catccttact ttacaatacc accgcactgc cagcggacga tgaagggtcc 180

aactatggat atggctccac cacaacgctc agtggcctcc agttcgagac ctataatatc 240

actgtgatga tgaactttag ctgtgacgac tatgaccttc tatcggagga catgtggtct 300

agtgcctact ttaagatcat cgtctacatg ctctacattc ccatctttat cttcgccctg 360

atcggcaacg gaacggtctg ctatatcgtc tattccacac ctcgcatgcg cacggtcacc 420

aattacttta tagccagctt ggccatcggc gacatcctga tgtccttctt ctgcgttccg 480

tcgtccttca tctcgctgtt catcctgaac tactggcctt ttggcctggc cctctgtcac 540

tttgtgaact actcgcaggc ggtctcagtt ctggtcagcg cctatacttt ggtggcaatt 600

agcattgacc gctacatagc cattatgtgg ccattaaagc cacgcatcac aaaacgctat 660

gccaccttca tcatcgccgg cgtttggttt attgcacttg ccaccgcact tcccataccc 720

atcgtctctg gactcgacat cccaatgtcg ccgtggcaca cgaaatgcga gaaatacatt 780

tgccgcgaaa tgtggccgtc gcggacgcag gagtactact acaccctgtc cctcttcgcg 840

ctgcagttcg tcgtgccgct gggcgtgctc atcttcacct acgcccggat caccattcgc 900

gtctgggcga aacgaccgcc aggcgaggcg gaaaccaacc gcgaccagcg gatggcacgc 960

tccaaacgga agatggtcaa aatgatgctg acggttgtga ttgtgttcac ctgctgttgg 1020

ctgcccttca atattttgca gcttttactg aacgacgagg agttcgccca ctgggatcct 1080

ctgccgtatg tgtggttcgc gtttcactgg ctggccatgt cgcactgctg ctacaatccg 1140

atcatctact gctacatgaa cgcccgtttc aggagcggat tcgtccagct gatgcaccgt 1200

atgcccggcc tgcgtcgctg gtgctgcctg cggagcgtcg gtgatcgcat gaacgcaact 1260

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aaaatatgca ttaggaacgg gtccagcact tcctctcaat cgaatgaaca catccaccac 1380

ctacatcagc gctcgtcgaa agccacgagc gacatctttg cgagcgaacc cattatcatg 1440

cggcgagacg tcaccactgc ggtagctgtc atatcaaaaa ataaaactga ttcaccggtg 1500

cgccgatcgg gaagctcagg tggaacagaa gcaaacataa gaagcaccga gttttg 1556

<210> 16
<211> 518
<212> PRT

<213> D. Melanogaster

<400> 16

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Met Glu His His Asn Ser His Leu Leu Pro Gly Gly Ser Glu Lys Met
1               5                  10                  15

Tyr Tyr Ile Ala His Gln Gln Pro Met Leu Arg Asn Glu Asp Asp Asn
            20                  25                  30

Tyr Gln Glu Gly Tyr Phe Ile Arg Pro Asp Pro Ala Ser Leu Leu Tyr
        35                  40                  45

Asn Thr Thr Ala Leu Pro Ala Asp Asp Glu Gly Ser Asn Tyr Gly Tyr
    50                  55                  60

Gly Ser Thr Thr Thr Leu Ser Gly Leu Gln Phe Glu Thr Tyr Asn Ile
65                  70                  75                  80

Thr Val Met Met Asn Phe Ser Cys Asp Asp Tyr Asp Leu Leu Ser Glu
                85                  90                  95

Asp Met Trp Ser Ser Ala Tyr Phe Lys Ile Ile Val Tyr Met Leu Tyr
            100                 105                 110

Ile Pro Ile Phe Ile Phe Ala Leu Ile Gly Asn Gly Thr Val Cys Tyr
        115                 120                 125

Ile Val Tyr Ser Thr Pro Arg Met Arg Thr Val Thr Asn Tyr Phe Ile
    130                 135                 140

Ala Ser Leu Ala Ile Gly Asp Ile Leu Met Ser Phe Phe Cys Val Pro
145                 150                 155                 160

Ser Ser Phe Ile Ser Leu Phe Ile Leu Asn Tyr Trp Pro Phe Gly Leu
                165                 170                 175

Ala Leu Cys His Phe Val Asn Tyr Ser Gln Ala Val Ser Val Leu Val
            180                 185                 190

Ser Ala Tyr Thr Leu Val Ala Ile Ser Ile Asp Arg Tyr Ile Ala Ile
        195                 200                 205

Met Trp Pro Leu Lys Pro Arg Ile Thr Lys Arg Tyr Ala Thr Phe Ile
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210 215 220

Ile Ala Gly Val Trp Phe Ile Ala Leu Ala Thr Ala Leu Pro Ile Pro
225 230 235 240

Ile Val Ser Gly Leu Asp Ile Pro Met Ser Pro Trp His Thr Lys Cys
245 250 255

Glu Lys Tyr Ile Cys Arg Glu Met Trp Pro Ser Arg Thr Gln Glu Tyr
260 265 270

Tyr Tyr Thr Leu Ser Leu Phe Ala Leu Gln Phe Val Val Pro Leu Gly
275 280 285

Val Leu Ile Phe Thr Tyr Ala Arg Ile Thr Ile Arg Val Trp Ala Lys
290 295 300

Arg Pro Pro Gly Glu Ala Glu Thr Asn Arg Asp Gln Arg Met Ala Arg
305 310 315 320

Ser Lys Arg Lys Met Val Lys Met Met Leu Thr Val Val Ile Val Phe
325 330 335

Thr Cys Cys Trp Leu Pro Phe Asn Ile Leu Gln Leu Leu Leu Asn Asp
340 345 350

Glu Glu Phe Ala His Trp Asp Pro Leu Pro Tyr Val Trp Phe Ala Phe
355 360 365

His Trp Leu Ala Met Ser His Cys Cys Tyr Asn Pro Ile Ile Tyr Cys
370 375 380

Tyr Met Asn Ala Arg Phe Arg Ser Gly Phe Val Gln Leu Met His Arg
385 390 395 400

Met Pro Gly Leu Arg Arg Trp Cys Cys Leu Arg Ser Val Gly Asp Arg
405 410 415

Met Asn Ala Thr Ser Gly Glu Met Thr Thr Lys Tyr His Arg His Val
420 425 430

Gly Asp Ala Leu Phe Arg Lys Pro Lys Ile Cys Ile Arg Asn Gly Ser
435 440 445

Ser Thr Ser Ser Gln Ser Asn Glu His Ile His His Leu His Gln Arg
450 455 460

Ser Ser Lys Ala Thr Ser Asp Ile Phe Ala Ser Glu Pro Ile Ile Met
465 470 475 480

Arg Arg Asp Val Thr Thr Ala Val Ala Val Ile Ser Lys Asn Lys Thr
485 490 495

Asp Ser Pro Val Arg Arg Ser Gly Ser Ser Gly Gly Thr Glu Ala Asn
500 505 510

Ile Arg Ser Thr Glu Phe
515

<210> 17
<211> 1628
<212> DNA
<213> D. melanogaster

<400> 17
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gaagcagaat ttgagcgtct atacgcggct cccgctgaga ttgtggccct gttgtccatt 120

ttctatgggg gaatcagtat cgtggccgtc attggcaaca ctttggtcat ctgggtggtg 180

gccacgacca ggcaaatgcg gaccgtgaca aatatgtata tcgctaattt ggcttttgcc 240

gatgtgatta ttggcctctt ctgcatacca tttcagttcc aggctgccct gctgcagagt 300

tggaacctgc cgtggttcat gtgcagcttc tgcccttcg tccaggccct gagtgtaaat 360

gtctcggtat tcacgctgac cgccattgca atcgatcggc atagggccat cattaatcca 420

cttagggcac gtcccaccaa gttcgtatcg aagttcataa ttggtggaat ttggatgctg 480

gccctgctat ttgcggtgcc ctttgccatt gcctttcgtg tggaggagtt gaccgaaaga 540

tttcgcgaga acaatgagac ctacaatgtg acgcggccat tctgcatgaa caagaaccta 600

tccgatgatc aattgcaatc ctttcgctac accctggttt ttgtgcagta tctggttcca 660

ttctgtgtca tcagctttgt ctacatccag atggcggtac gattgtgggg cacacgtgct 720

cctggtaacg cacaggattc acgggacata acgctgttga aaaacaagaa gaaggtcatc 780

aaaatgctga ttatcgtggt cattatcttt ggactctgct ggctgccact gcagctctat 840

aatattctgt atgtcacgat accggaaatc aacgactacc acttcattag catcgtctgg 900

ttttgctgcg attggctggc catgagcaat agctgctaca atccctttat ttatggcatc 960

tacaatgaaa aatttaagcg ggaattcaac aagcgatttg cggcctgttt ctgcaagttc 1020

aagacgagca tggacgccca cgaaaggacc ttttcgatgc acacccgcgc cagctccata 1080

aggtcaacct acgccaactc ctcgatgcga atccggagta atctctttgg tccggcgcgt 1140

ggtggtgtca acaatgggaa gccgggcttg catatgccgc gggtgcatgg atccggtgct 1200

aacagcggca tttacaacgg aagtagtggg cagaacaaca atgtcaatgg ccaacatcat 1260

cagcatcaaa gcgtggttac ctttgcggcc actccgggtg tttcggcacc aggtgttggc 1320

gttgcaatgc cgccgtggcg gcgaaacaac ttcaaacctc tgcatccgaa cgtaatcgaa 1380

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gcatccgggg ccggagtcca gttggccctg ctaagcaggg agagctccag ctgcatttgc 1500

gaacaggaat ttggcagcca aaccgaatgc gatggcacct gcatactcag cgaggtgtcg 1560

cgagtccacc tgcccggctc gcaggcgaag gacaaggatg cgggcaagtc cttgtggcaa 1620

ccacttta 1628

<210> 18
<211> 542
<212> PRT
<213> D. melanogaster

<400> 18

Met Ala Met Asp Leu Ile Glu Gln Glu Ser Arg Leu Glu Phe Leu Pro
1 5 10 15

Gly Ala Glu Glu Glu Ala Glu Phe Glu Arg Leu Tyr Ala Ala Pro Ala
20 25 30

Glu Ile Val Ala Leu Leu Ser Ile Phe Tyr Gly Gly Ile Ser Ile Val
35 40 45

Ala Val Ile Gly Asn Thr Leu Val Ile Trp Val Val Ala Thr Thr Arg
50 55 60

Gln Met Arg Thr Val Thr Asn Met Tyr Ile Ala Asn Leu Ala Phe Ala
65 70 75 80

Asp Val Ile Ile Gly Leu Phe Cys Ile Pro Phe Gln Phe Gln Ala Ala
85 90 95

Leu Leu Gln Ser Trp Asn Leu Pro Trp Phe Met Cys Ser Phe Cys Pro
100 105 110

Phe Val Gln Ala Leu Ser Val Asn Val Ser Val Phe Thr Leu Thr Ala
115 120 125

Ile Ala Ile Asp Arg His Arg Ala Ile Ile Asn Pro Leu Arg Ala Arg
130 135 140

Pro Thr Lys Phe Val Ser Lys Phe Ile Ile Gly Gly Ile Trp Met Leu
145 150 155 160

Ala Leu Leu Phe Ala Val Pro Phe Ala Ile Ala Phe Arg Val Glu Glu
165 170 175

Leu Thr Glu Arg Phe Arg Glu Asn Asn Glu Thr Tyr Asn Val Thr Arg
180 185 190

Pro Phe Cys Met Asn Lys Asn Leu Ser Asp Asp Gln Leu Gln Ser Phe
195 200 205

Arg Tyr Thr Leu Val Phe Val Gln Tyr Leu Val Pro Phe Cys Val Ile
210 215 220

Ser Phe Val Tyr Ile Gln Met Ala Val Arg Leu Trp Gly Thr Arg Ala
225 230 235 240

Pro Gly Asn Ala Gln Asp Ser Arg Asp Ile Thr Leu Leu Lys Asn Lys
245 250 255

Lys Lys Val Ile Lys Met Leu Ile Ile Val Val Ile Ile Phe Gly Leu
260 265 270

Cys Trp Leu Pro Leu Gln Leu Tyr Asn Ile Leu Tyr Val Thr Ile Pro
275 280 285

Glu Ile Asn Asp Tyr His Phe Ile Ser Ile Val Trp Phe Cys Cys Asp
290 295 300

Trp Leu Ala Met Ser Asn Ser Cys Tyr Asn Pro Phe Ile Tyr Gly Ile
305 310 315 320

Tyr Asn Glu Lys Phe Lys Arg Glu Phe Asn Lys Arg Phe Ala Ala Cys
325 330 335

Phe Cys Lys Phe Lys Thr Ser Met Asp Ala His Glu Arg Thr Phe Ser
340 345 350

Met His Thr Arg Ala Ser Ser Ile Arg Ser Thr Tyr Ala Asn Ser Ser
355 360 365

Met Arg Ile Arg Ser Asn Leu Phe Gly Pro Ala Arg Gly Gly Val Asn
370 375 380

Asn Gly Lys Pro Gly Leu His Met Pro Arg Val His Gly Ser Gly Ala
385 390 395 400

Asn Ser Gly Ile Tyr Asn Gly Ser Ser Gly Gln Asn Asn Asn Val Asn
405 410 415

Gly Gln His His Gln His Gln Ser Val Val Thr Phe Ala Ala Thr Pro
420 425 430

Gly Val Ser Ala Pro Gly Val Gly Val Ala Met Pro Pro Trp Arg Arg
435 440 445

Asn Asn Phe Lys Pro Leu His Pro Asn Val Ile Glu Cys Glu Asp Asp
450 455 460

Val Ala Leu Met Glu Leu Pro Ser Thr Thr Pro Pro Ser Glu Glu Leu
465 470 475 480

Ala Ser Gly Ala Gly Val Gln Leu Ala Leu Leu Ser Arg Glu Ser Ser
485 490 495

Ser Cys Ile Cys Glu Gln Glu Phe Gly Ser Gln Thr Glu Cys Asp Gly
500 505 510

Thr Cys Ile Leu Ser Glu Val Ser Arg Val His Leu Pro Gly Ser Gln
515 520 525

Ala Lys Asp Lys Asp Ala Gly Lys Ser Leu Trp Gln Pro Leu
530 535 540

<210> 19
<211> 1451
<212> DNA
<213> D. melanogaster

<400> 19
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tcagaggcaa atgccacaaa ttggtataac acgaacgaga gcttatatac cacggaactg 120

aaccatagat ggattagtgg tagttccaca attcagccag aggagtccct ttatggcact 180

gatttgccca cctatcaaca ttgcatagcc acgcggaatt cctttgctga cttgttcact 240

gtggtgctct acggatttgt gtgcattatc ggattatttg gcaacaccct ggtgatctac 300

gtggtgttgc gcttttccaa aatgcaaacg gtcacgaata tatatatcct gaatctggcg 360

gtggcagacg agtgcttcct gattggaata ccctttctgc tgtacacaat gcgaatttgc 420

agctggcgat tcggggagtt tatgtgcaaa gcctacatgg tgagcacatc catcacctcc 480

ttcacctcgt cgatttttct gctcatcatg tccgcggatc gatatatagc ggtatgccac 540

ccgatttcct cgccacgata tcgaactctg catattgcca aagtggtctc agcgattgcc 600

tggtcaactt cagcggtcct catgctgccc gtgatccttt atgccagcac tgtggagcag 660

gaggatggca tcaattactc gtgcaacata atgtggccag atgcgtacaa gaagcattcg 720

ggcaccacct tcatactgta cacatttttc ctaggattcg ccacaccgct gtgctttatc 780

ctgagtttct actacttggt tataaggaaa ctgcgatcgg tgggtcccaa accaggaacg 840

aagtccaagg agaagaggcg ggctcacagg aaggtcactc gactggtact gacggtgata 900

agtgtataca ttctatgttg gctccctcac tggatttctc aggtggccct gattcactcg 960

aatcccgcgc aaagggacct ctcccgactg gaaatactca ttttcctact tctgggggca 1020

ctggtttact cgaattcggc ggtgaatccc atactttatg ccttcctaag tgagaacttc 1080

cggaagagct tcttcaaggc ctttacctgt atgaataagc aggatatcaa cgctcaactc 1140

cagctggagc ccagtgtttt caccaaacag ggcagtaaaa agaggggtgg ctccaagcgc 1200

ctgttgacca gcaatccgca gattcctcca ctgctgccac tgaatgcggg taacaacaat 1260

tcatcgacca ccacatcctc gaccacgaca gcggaaaaga ccggaaccac ggggacacag 1320

aaatcatgca attccaatgg caaagtgaca gctccgccgg agaatttgat tatatgtttg 1380

agcgagcagc aggaggcatt ttgcaccacc gcgagaagag gatcgggcgc agtgcagcag 1440

acagatttgt a 1451

<210> 20
<211> 483
<212> PRT
<213> D. melanogaster

<400> 20

Met Phe Thr Trp Leu Met Met Asp Val Leu Gln Phe Val Lys Gly Glu
1 5 10 15

Met Thr Ala Asp Ser Glu Ala Asn Ala Thr Asn Trp Tyr Asn Thr Asn
20 25 30

Glu Ser Leu Tyr Thr Thr Glu Leu Asn His Arg Trp Ile Ser Gly Ser
35 40 45

Ser Thr Ile Gln Pro Glu Glu Ser Leu Tyr Gly Thr Asp Leu Pro Thr
50 55 60

Tyr Gln His Cys Ile Ala Thr Arg Asn Ser Phe Ala Asp Leu Phe Thr
65 70 75 80

Val Val Leu Tyr Gly Phe Val Cys Ile Ile Gly Leu Phe Gly Asn Thr
85 90 95

Leu Val Ile Tyr Val Val Leu Arg Phe Ser Lys Met Gln Thr Val Thr
100 105 110

Asn Ile Tyr Ile Leu Asn Leu Ala Val Ala Asp Glu Cys Phe Leu Ile
115 120 125

Gly Ile Pro Phe Leu Leu Tyr Thr Met Arg Ile Cys Ser Trp Arg Phe
130 135 140

Gly Glu Phe Met Cys Lys Ala Tyr Met Val Ser Thr Ser Ile Thr Ser
145 150 155 160

Phe Thr Ser Ser Ile Phe Leu Leu Ile Met Ser Ala Asp Arg Tyr Ile
165 170 175

Ala Val Cys His Pro Ile Ser Ser Pro Arg Tyr Arg Thr Leu His Ile
180 185 190

Ala Lys Val Val Ser Ala Ile Ala Trp Ser Thr Ser Ala Val Leu Met
195 200 205

Leu Pro Val Ile Leu Tyr Ala Ser Thr Val Glu Gln Glu Asp Gly Ile
210 215 220

Asn Tyr Ser Cys Asn Ile Met Trp Pro Asp Ala Tyr Lys Lys His Ser
225 230 235 240

Gly Thr Thr Phe Ile Leu Tyr Thr Phe Phe Leu Gly Phe Ala Thr Pro
245 250 255

Leu Cys Phe Ile Leu Ser Phe Tyr Tyr Leu Val Ile Arg Lys Leu Arg
260 265 270

Ser Val Gly Pro Lys Pro Gly Thr Lys Ser Lys Glu Lys Arg Arg Ala
275 280 285

His Arg Lys Val Thr Arg Leu Val Leu Thr Val Ile Ser Val Tyr Ile
290 295 300

Leu Cys Trp Leu Pro His Trp Ile Ser Gln Val Ala Leu Ile His Ser
305 310 315 320

Asn Pro Ala Gln Arg Asp Leu Ser Arg Leu Glu Ile Leu Ile Phe Leu
325 330 335

Leu Leu Gly Ala Leu Val Tyr Ser Asn Ser Ala Val Asn Pro Ile Leu
340 345 350

Tyr Ala Phe Leu Ser Glu Asn Phe Arg Lys Ser Phe Phe Lys Ala Phe
355 360 365

Thr Cys Met Asn Lys Gln Asp Ile Asn Ala Gln Leu Gln Leu Glu Pro
370 375 380

Ser Val Phe Thr Lys Gln Gly Ser Lys Lys Arg Gly Gly Ser Lys Arg
385 390 395 400

Leu Leu Thr Ser Asn Pro Gln Ile Pro Pro Leu Leu Pro Leu Asn Ala
405 410 415

Gly Asn Asn Asn Ser Ser Thr Thr Thr Ser Ser Thr Thr Thr Ala Glu
420 425 430

Lys Thr Gly Thr Thr Gly Thr Gln Lys Ser Cys Asn Ser Asn Gly Lys
435 440 445

Val Thr Ala Pro Pro Glu Asn Leu Ile Ile Cys Leu Ser Glu Gln Gln
450 455 460

Glu Ala Phe Cys Thr Thr Ala Arg Arg Gly Ser Gly Ala Val Gln Gln
465 470 475 480

Thr Asp Leu

<210> 21
<211> 1754
<212> DNA
<213> D. melanogaster

<400> 21
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aacgtggcac cctacaatgg aactggaaac ggaggcactg tctccttggc gggcaatgcg 180

acaagcagct atggcgatga tgatagggat ggctatatgg acaccgagcc cagtgacctg 240

gtcaccgaac tggccttctc cctgggcacc agttcaagtc caagtcccag ttccacaccc 300

gcttccagct ccagtacttc cactggcatg cccgtctggc tgatacccag ctatagcatg 360

attctgctgt tcgccgtgct gggcaacctg ctggtcatct cgacgctggt gcagaatcgc 420

cggatgcgta ccataaccaa cgtgttcctg ctcaacctgg ccatatcgga catgctgctg 480

ggcgtgctct gcatgcccgt caccctggtg ggcaccctgc tgcgaaactt catctttggc 540

gagttcctct gcaagctctt tcagttctcg caagccgcct ccgtggccgt ttcgtcctgg 600

accttggtgg ccatatcctg tgagcgctac tacgcgatat gccatccact gcgctcgcga 660

tcctggcaga caatcagtca cgcctacaag atcatcggct tcatctggct gggcggcatc 720

ctctgcatga cgcccatagc ggtctttagt caattgatac ccaccagtcg accgggctac 780

tgcaagtgcc gtgagttttg gcccgaccag ggatacgagc tcttctacaa catcctgctg 840

gacttcctgc tgctcgtcct gccgcttctc gtcctctgcg tggcctacat cctcatcacg 900

cgtaccctgt acgtaggcat ggccaaggac agcggacgca tcctgcagca atcgctgcct 960

gtttccgcta caacggccgg cggaagcgca ccgaatccgg gcaccagcag cagtagtaac 1020

tgcatcctgg tcctgaccgc caccgcagtc tataatgaaa atagtaacaa taataatgga 1080

aattcagagg gatccgcagg cggaggatca accaatatgg caacgaccac cttgacaacg 1140

agaccaacgg ctccaactgt gatcaccacc accacgacga ccacggtgac gctggccaag 1200

acctcctcgc ccagcattcg cgtccacgat gcggcacttc gcaggtccaa cgaggccaag 1260

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atctgctgga ctccgctgta cgtgatcaac acgatggtca tgctgatcgg accggtggtg 1380

tacgagtatg tcgactacac ggccatcagt ttcctccagc tgctggccta ctcatccagc 1440

tgctgcaatc cgatcaccta ctgcttcatg aacgccagct tccggcgcgc ctttgtcgac 1500

accttcaagg gtctgccctg gcgtcgtgga gcaggtgcca gcggaggcgt cggtggtgct 1560

gctggtggag gactctccgc cagccaggcg ggcgcaggcc cgggcgccta tgcgagtgcc 1620

aacaccaaca ttagtctcaa tcccggccta gccatgggta tgggcacctg gcggagtcgc 1680

tcacgccacg agtttctcaa tgcggtggtg accaccaata gtgccgccgc cgccgtcaac 1740

agtcctcagc tcta 1754

<210> 22
<211> 584
<212> PRT
<213> D. melanogaster

<400> 22

Met Phe Asn Tyr Glu Glu Gly Asp Ala Asp Gln Ala Ala Met Ala Ala
1 5 10 15

Ala Ala Ala Tyr Arg Ala Leu Leu Asp Tyr Tyr Ala Asn Ala Pro Ser
20 25 30

Ala Ala Gly His Ile Val Ser Leu Asn Val Ala Pro Tyr Asn Gly Thr
35 40 45

Gly Asn Gly Gly Thr Val Ser Leu Ala Gly Asn Ala Thr Ser Ser Tyr
50 55 60

Gly Asp Asp Asp Arg Asp Gly Tyr Met Asp Thr Glu Pro Ser Asp Leu
65 70 75 80

Val Thr Glu Leu Ala Phe Ser Leu Gly Thr Ser Ser Ser Pro Ser Pro
85 90 95

Ser Ser Thr Pro Ala Ser Ser Ser Ser Thr Ser Thr Gly Met Pro Val
100 105 110

Trp Leu Ile Pro Ser Tyr Ser Met Ile Leu Leu Phe Ala Val Leu Gly
115 120 125

Asn Leu Leu Val Ile Ser Thr Leu Val Gln Asn Arg Arg Met Arg Thr
130 135 140

Ile Thr Asn Val Phe Leu Leu Asn Leu Ala Ile Ser Asp Met Leu Leu
145 150 155 160

Gly Val Leu Cys Met Pro Val Thr Leu Val Gly Thr Leu Leu Arg Asn
165 170 175

Phe Ile Phe Gly Glu Phe Leu Cys Lys Leu Phe Gln Phe Ser Gln Ala
180 185 190

Ala Ser Val Ala Val Ser Ser Trp Thr Leu Val Ala Ile Ser Cys Glu
195 200 205

Arg Tyr Tyr Ala Ile Cys His Pro Leu Arg Ser Arg Ser Trp Gln Thr
210 215 220

Ile Ser His Ala Tyr Lys Ile Ile Gly Phe Ile Trp Leu Gly Gly Ile
225 230 235 240

Leu Cys Met Thr Pro Ile Ala Val Phe Ser Gln Leu Ile Pro Thr Ser
245 250 255

Arg Pro Gly Tyr Cys Lys Cys Arg Glu Phe Trp Pro Asp Gln Gly Tyr
260 265 270

Glu Leu Phe Tyr Asn Ile Leu Leu Asp Phe Leu Leu Leu Val Leu Pro
275 280 285

Leu Leu Val Leu Cys Val Ala Tyr Ile Leu Ile Thr Arg Thr Leu Tyr
290 295 300

Val Gly Met Ala Lys Asp Ser Gly Arg Ile Leu Gln Gln Ser Leu Pro
305 310 315 320

Val Ser Ala Thr Thr Ala Gly Gly Ser Ala Pro Asn Pro Gly Thr Ser
325 330 335

Ser Ser Ser Asn Cys Ile Leu Val Leu Thr Ala Thr Ala Val Tyr Asn
340 345 350

Glu Asn Ser Asn Asn Asn Asn Gly Asn Ser Glu Gly Ser Ala Gly Gly
355 360 365

Gly Ser Thr Asn Met Ala Thr Thr Thr Leu Thr Thr Arg Pro Thr Ala
370 375 380

Pro Thr Val Ile Thr Thr Thr Thr Thr Thr Thr Val Thr Leu Ala Lys
385 390 395 400

Thr Ser Ser Pro Ser Ile Arg Val His Asp Ala Ala Leu Arg Arg Ser
405 410 415

Asn Glu Ala Lys Thr Leu Glu Ser Lys Lys Arg Val Val Lys Met Leu
420 425 430

Phe Val Leu Val Leu Glu Phe Phe Ile Cys Trp Thr Pro Leu Tyr Val
435 440 445

Ile Asn Thr Met Val Met Leu Ile Gly Pro Val Val Tyr Glu Tyr Val
450 455 460

Asp Tyr Thr Ala Ile Ser Phe Leu Gln Leu Leu Ala Tyr Ser Ser Ser
465 470 475 480

Cys Cys Asn Pro Ile Thr Tyr Cys Phe Met Asn Ala Ser Phe Arg Arg
485 490 495

Ala Phe Val Asp Thr Phe Lys Gly Leu Pro Trp Arg Arg Gly Ala Gly
500 505 510

Ala Ser Gly Gly Val Gly Gly Ala Ala Gly Gly Gly Leu Ser Ala Ser
515 520 525

Gln Ala Gly Ala Gly Pro Gly Ala Tyr Ala Ser Ala Asn Thr Asn Ile
530 535 540

Ser Leu Asn Pro Gly Leu Ala Met Gly Met Gly Thr Trp Arg Ser Arg

545 550 555 560

Ser Arg His Glu Phe Leu Asn Ala Val Val Thr Thr Asn Ser Ala Ala
565 570 575

Ala Ala Val Asn Ser Pro Gln Leu
580

<210> 23
<211> 1452
<212> DNA
<213> D. melanogaster

<400> 23
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gagggtctgg cactggatat gggccacaat gccagcgccg acggcggaat agtaccgtat 180

gtgcccgtgc tggaccgccc ggagacgtac attgtcaccg tgctgtacac gctcatcttc 240

attgtgggag ttttgggcaa cggcacgctg gtcatcatct tctttcgcca ccgctccatg 300

cgcaacatac ccaacacata cattctttca ctggccctgg ctgatctgtt ggttatattg 360

gtgtgtgtac ctgtggccac gattgtctac acgcaggaaa gctggccctt tgagcggaac 420

atgtgccgca tcagcgagtt ctttaaggac atatccatcg gggtgtccgt gtttacactg 480

accgcccttt ccggcgagcg gtactgcgcc attgtaaatc ccctacgcaa gcttcagacc 540

aagccgctca ctgtctttac tgcggtgatg atctggatcc tggccatcct actgggcatg 600

ccttcggttc ttttctccga catcaagtcc taccctgtgt tcacagccac cggtaacatg 660

accattgaag tgtgctcccc atttcgcgac ccggagtatg caaagttcat ggtggcgggc 720

aaggcactgg tgtactacct gttgccgctg tccatcattg gggcgctata catcatgatg 780

gccaagcggc tccatatgag cgcccgcaac atgcccggcg aacagcagag catgcagagc 840

cgcacccagg ctagggcccg actccatgtg gcgcgcatgg tggtagcatt cgtggtggtg 900

ttcttcatct gcttcttccc gtaccacgtg tttgagctgt ggtaccactt ctacccaacg 960

gctgaggagg acttcgatga gttctggaac gtgctgcgca tccttcctaa actcgtgcgt 1020

caaccccgtg gcctctactg cgtgtccggg gtgtttcggc agcactttaa tcgctacctc 1080

tgctgcatct gcgtcaagcg gcagccgcac ctgcggcagc actcaacggc cactggaatg 1140

atggacaata ccagtgtgat gtccatgcgc cgctccacgt acgtgggtgg aaccgctggc 1200

aatctgcggg cctcgctgca ccggaacagc aatcacggag ttggtggagc tggaggtgga 1260

gtaggaggag gagtagggtc aggtcgtgtg ggcagctttc atcggcagga ctcgatgccc 1320

ctgcagcacg gaaatgccca cggaggtggt gcgggcgggg gatcctccgg acttggagcc 1380

ggcgggcgga cggcggcagt gagcgaaaag agctttataa atcgttacga aagtggcgta 1440

atgcgctact aa 1452

<210> 24
<211> 483
<212> PRT
<213> D. melanogaster

<400> 24

Met Tyr Ala Ser Leu Met Asp Val Gly Gln Thr Leu Ala Ala Arg Leu
1 5 10 15

Ala Asp Ser Asp Gly Asn Gly Ala Asn Asp Ser Gly Leu Leu Ala Thr
20 25 30

Gly Gln Gly Leu Glu Gln Glu Gln Glu Gly Leu Ala Leu Asp Met Gly
35 40 45

His Asn Ala Ser Ala Asp Gly Gly Ile Val Pro Tyr Val Pro Val Leu
50 55 60

Asp Arg Pro Glu Thr Tyr Ile Val Thr Val Leu Tyr Thr Leu Ile Phe
65 70 75 80

Ile Val Gly Val Leu Gly Asn Gly Thr Leu Val Ile Ile Phe Phe Arg
85 90 95

His Arg Ser Met Arg Asn Ile Pro Asn Thr Tyr Ile Leu Ser Leu Ala
100 105 110

Leu Ala Asp Leu Leu Val Ile Leu Val Cys Val Pro Val Ala Thr Ile
115 120 125

Val Tyr Thr Gln Glu Ser Trp Pro Phe Glu Arg Asn Met Cys Arg Ile
130 135 140

Ser Glu Phe Phe Lys Asp Ile Ser Ile Gly Val Ser Val Phe Thr Leu
145 150 155 160

Thr Ala Leu Ser Gly Glu Arg Tyr Cys Ala Ile Val Asn Pro Leu Arg
165 170 175

Lys Leu Gln Thr Lys Pro Leu Thr Val Phe Thr Ala Val Met Ile Trp
180 185 190

Ile Leu Ala Ile Leu Leu Gly Met Pro Ser Val Leu Phe Ser Asp Ile
195 200 205

Lys Ser Tyr Pro Val Phe Thr Ala Thr Gly Asn Met Thr Ile Glu Val
210 215 220

Cys Ser Pro Phe Arg Asp Pro Glu Tyr Ala Lys Phe Met Val Ala Gly
225 230 235 240

Lys Ala Leu Val Tyr Tyr Leu Leu Pro Leu Ser Ile Ile Gly Ala Leu
245 250 255

Tyr Ile Met Met Ala Lys Arg Leu His Met Ser Ala Arg Asn Met Pro
260 265 270

Gly Glu Gln Gln Ser Met Gln Ser Arg Thr Gln Ala Arg Ala Arg Leu
275 280 285

His Val Ala Arg Met Val Val Ala Phe Val Val Val Phe Phe Ile Cys
290 295 300

Phe Phe Pro Tyr His Val Phe Glu Leu Trp Tyr His Phe Tyr Pro Thr
305 310 315 320

Ala Glu Glu Asp Phe Asp Glu Phe Trp Asn Val Leu Arg Ile Leu Pro
325 330 335

Lys Leu Val Arg Gln Pro Arg Gly Leu Tyr Cys Val Ser Gly Val Phe
340 345 350

Arg Gln His Phe Asn Arg Tyr Leu Cys Cys Ile Cys Val Lys Arg Gln
355 360 365

Pro His Leu Arg Gln His Ser Thr Ala Thr Gly Met Met Asp Asn Thr
370 375 380

Ser Val Met Ser Met Arg Arg Ser Thr Tyr Val Gly Gly Thr Ala Gly
385 390 395 400

Asn Leu Arg Ala Ser Leu His Arg Asn Ser Asn His Gly Val Gly Gly
405 410 415

Ala Gly Gly Gly Val Gly Gly Gly Val Gly Ser Gly Arg Val Gly Ser
420 425 430

Phe His Arg Gln Asp Ser Met Pro Leu Gln His Gly Asn Ala His Gly
435 440 445

Gly Gly Ala Gly Gly Gly Ser Ser Gly Leu Gly Ala Gly Gly Arg Thr
450 455 460

Ala Ala Val Ser Glu Lys Ser Phe Ile Asn Arg Tyr Glu Ser Gly Val
465 470 475 480

Met Arg Tyr

<210> 25
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 25

Thr Asp Val Asp His Val Phe Leu Arg Phe
1 5 10

<210> 26
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 26

Asp Pro Lys Gln Asp Phe Met Arg Phe
1 5

<210> 27

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 27

Pro Asp Asn Phe Met Arg Phe
1 5

<210> 28
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 28

Thr Pro Ala Glu Asp Phe Met Arg Phe
1 5

<210> 29
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 29

Ser Leu Lys Gln Asp Phe Met His Phe
1 5

<210> 30
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 30

Ser Val Lys Gln Asp Phe Met His Phe
1 5

<210> 31
<211> 6

<212> PRT
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<220>
<223> Novel Sequence

<400> 31

Ala Ala Met Asp Arg Tyr
1 5

<210> 32
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 32

Ser Val Gln Asp Asn Phe Met His Phe
1 5

<210> 33
<211> 10
<212> PRT
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<400> 33

Ala Arg Gly Pro Gln Leu Arg Leu Arg Phe
1 5 10

<210> 34
<211> 10
<212> PRT
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<220>
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<400> 34

Gly Asp Gly Arg Leu Tyr Ala Phe Gly Leu
1 5 10

<210> 35
<211> 8
<212> PRT

<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 35

Asp Arg Leu Tyr Ser Phe Gly Leu
1 5

<210> 36
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 36

Ala Pro Ser Gly Ala Gln Arg Leu Tyr Gly Phe Gly Leu
1 5 10

<210> 37
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 37

Gly Gly Ser Leu Tyr Ser Phe Gly Leu
1 5

<210> 38
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 38

Phe Ile Arg Phe
1

<210> 39
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 39

Lys Asn Glu Phe Ile Arg Phe
1 5

<210> 40
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 40

Phe Met Arg Phe
1

<210> 41
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 41

Lys Ser Ala Phe Met Arg Phe
1 5

<210> 42
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 42

Lys Pro Asn Phe Leu Arg Phe
1 5

<210> 43
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 43

Phe Leu Arg Phe
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<210> 44
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 44

Tyr Leu Arg Phe
1

<210> 45
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 45

Lys Pro Asn Phe Leu Arg Tyr
1 5

<210> 46
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 46

Thr Asn Arg Asn Phe Leu Arg Phe
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<210> 47
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 47

Arg Asn Lys Phe Glu Phe Ile Arg Phe
1 5

<210> 48
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 48

Ala Gly Pro Arg Phe Ile Arg Phe
1 5

<210> 49
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<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 49

Gly Leu Gly Pro Arg Pro Leu Arg Phe
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<213> Artificial Sequence

<220>
<223> Novel Sequence

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<400> 50

Ile Leu Xaa Arg Phe
1 5

<210> 51

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 51

Ala Gly Ala Lys Phe Ile Arg Phe
1 5

<210> 52
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 52

Ala Pro Lys Pro Lys Phe Ile Arg Phe
1 5

<210> 53
<211> 8
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<213> Artificial Sequence

<220>
<223> Novel Sequence

<400> 53

Lys Ser Ala Phe Val Leu Arg Phe
1 5

<210> 54
<211> 9
<212> PRT
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<220>
<223> Novel Sequence

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Thr Lys Phe Gln Asp Phe Leu Arg Phe
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Ser Ala Glu Pro Phe Gly Thr Met Arg Phe
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Ala Ser Glu Asp Ala Leu Phe Gly Thr Met Arg Phe
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Ala Gly Ala Lys Phe Ile Arg Phe
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Lys Asn Glu Phe Ile Arg Phe
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Asn Gly Ala Pro Gln Pro Phe Val Arg Phe
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Arg Asn Lys Phe Glu Phe Ile Arg Phe
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Lys His Glu Tyr Leu Arg Phe
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Lys Ser Ala Phe Val Arg Phe
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Lys Ser Gln Tyr Ile Arg Phe
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Glu Ile Pro Gly Val Leu Arg Phe
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Ala Ser Trp Ala Ser Ser Val Arg Phe

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Ala Met Met Arg Phe
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Gly Leu Gly Pro Arg Pro Leu Arg Phe
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Phe Ile Arg Phe
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Gly Asp Val Pro Gly Val Leu Arg Phe
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Ser Asp Ile Gly Ile Ser Glu Pro Asn Phe Leu Arg Phe
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Ser Gly Lys Pro Thr Phe Ile Arg Phe
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Ala Glu Gly Leu Ser Ser Pro Leu Ile Arg Phe
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Phe Asp Arg Asp Phe Met Arg Phe
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Ala Gly Pro Arg Phe Ile Arg Phe
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Lys Pro Asn Phe Ile Arg Phe
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Phe Met Arg Phe
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Phe Leu Arg Phe
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Gly Asn Ser Phe Leu Arg Phe
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Asp Pro Ser Phe Leu Arg Phe
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Xaa Gln Asp Phe Met Arg Phe
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Ala Ala Met Asp Arg Tyr
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Ser Pro Lys Gln Asp Phe Met Arg Phe
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Pro Asp Asn Phe Met Arg Phe
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Asp Pro Lys Gln Asp Phe Met Arg Phe
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Thr Pro Ala Glu Asp Phe Met Arg Phe
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Tyr Leu Arg Phe
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Phe Leu Phe Gln Pro Gln Arg Phe
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Phe Asp Asp Tyr Gly His Leu Arg Phe
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Phe Asp Asp Tyr Gly His Leu Arg Phe
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Met Asp Ser Asn Phe Ile Arg Phe
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Phe Asp Asp Tyr Gly His Leu Arg Phe
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Phe Asp Asp Tyr Gly His Leu Arg Phe
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Phe Asp Asp Tyr Gly His Met Arg Phe
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Phe Asp Asp Tyr Gly His Met Arg Phe
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Gly Gly Asp Asp Gln Phe Asp Asp Tyr Gly His Met Arg Phe
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Asp Tyr Gly His Met Arg Phe
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Val Glu Arg Tyr Ala Phe Gly Leu
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Leu Pro Val Tyr Asn Phe Gly Leu
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Ser Arg Pro Tyr Ser Phe Gly Leu
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Glu Asp Val Asp His Val Phe Leu Arg Phe
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Ala Pro Thr Ser Ser Phe Ile Gly Met Arg
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Ala Pro Leu Ala Phe Tyr Gly Met Arg
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Ala Pro Leu Ala Phe Tyr Gly Leu Arg

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Gly Ser Gly Phe Ser Ser Trp Gly
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Gly Ser Ala Phe Tyr Ser Trp Gly
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Asn Pro Phe His Ser Trp Gly
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Pro Ser Phe His Ser Trp Ser
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<400> 181

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<223> Xaa is pGlu

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Xaa Arg Phe His Ser Trp Gly
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Gln Arg Phe His Ser Trp Gly
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Xaa Val Arg Phe Arg Gln Cys Tyr Phe Asn Pro Ile Ser Cys Phe
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Ala Gln Arg Ser Pro Ser Leu Arg Leu Arg Phe
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Pro Ile Arg Ser Pro Ser Leu Arg Leu Arg Phe
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<212> DNA
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<210> 189
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<400> 189
gccgccatga atcagacgga gcccgcccag c 31

<210> 190
<211> 28
<212> DNA
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<400> 190
gtattaccgc ggcatcagct tggtgacc 28

<210> 191
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<223> internal primer for D. melanogaster G protein-coupled receptor

<400> 191
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<223> Novel Sequence

<400> 192
attgcgagca gtgcgcatga tgggc 25

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<210> 194
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<210> 195
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<400> 195
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<210> 196
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<400> 197
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<210> 202
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<400> 205
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<400> 207
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<400> 208
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<400> 209
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<210> 210
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<210> 211
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<210> 212
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<400> 213
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<400> 214
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<210> 215
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<400> 215
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<400> 218
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<210> 219
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<400> 219
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<400> 220
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<400> 221
gtattagagc tgaggactgt tgacggcg 28

<210> 222
<211> 25
<212> DNA
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<400> 222
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<210> 223
<211> 25
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<220>
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<400> 223
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<210> 224

<211> 31
<212> DNA
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<220>
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<400> 224
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<210> 225
<211> 25
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<220>
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<400> 225
ttagagcatt tcaatattgg acgtt 25

<210> 226
<211> 25
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<400> 226
cccgtgacta gcatgtccct gcgaa 25

<210> 227
<211> 25
<212> DNA
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<220>
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<400> 227
accggaatcg cagtcgtcac aatcg 25

<210> 228
<211> 35
<212> DNA
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<220>
<223> Primer for D. melanogaster G protein-coupled receptor

<400> 228
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<210> 229
<211> 28
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<400> 229
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<400> 230

Asp Tyr Gly His Leu Arg Phe
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<210> 231
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<400> 231

Gly Ala Ser Phe Tyr Ser Trp Gly
1 5

<210> 232
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<400> 232

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